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GenCore version 5.1.6

QM protein = protein search - using sw model

July 28, 2004, 11:26:10 ; Search time 14 Seconds
(without alignments)
799,649 Million cell updates/sec

US-10-028-072-4

1132

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Gapop 10.0 , Gapext 0.5

Sequences searched: 141681 seqs, 52070155 residues

total number of hits satisfying chosen parameters: 141681

Maximum Match 100%

Sri Sannatai 13

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by normalizing the total number of predictions.

SUMMARIES

Questo risultato è stato ottenuto con un'algoritmo di apprendimento automatico.

NO.	Score	MACC1	Length	DB ID	Description
1	1087	.96.0	233	1	MTRP_HUMAN
2	1061	93.7	233	1	MTRP_MOUSE
3	191	16.9	262	1	LAM5_HUMAN
4	189.5	16.7	261	1	LAM5_MOUSE
5	103.5	9.1	385	1	G22C_DROME
6	93	8.2	413	1	Y567_BUCAP
7	90	8.0	274	1	NU2M_DROMA
8	89.5	7.9	446	1	D3DR_MOUSE
9	89.5	7.9	446	1	D3DR_RAT
10	88	7.8	551	1	FIXN_AZOCA
11	87.5	7.7	432	1	Y672_METJA
12	87.5	7.7	535	1	YDW6_SCHPO
13	87	7.7	341	1	NU2M_DROME
14	87	7.7	2253	1	PKDR_HUMAN
15	86.5	7.6	112	1	YUW4_CAEEL
16	86.5	7.6	1163	1	KCH2_RAT
17	85.5	7.6	341	1	NU2M_DROYA
18	85.5	7.6	379	1	CYB_TRASR
19	85.5	7.6	457	1	YG90_HAEIN
20	85.5	7.6	570	1	NU5M_PARTE
21	85	7.5	379	1	CYB_CAMBA
22	85	7.5	695	1	CIO4_HUMAN
23	84.5	7.5	267	1	CYB_ZAKOCU
24	84.5	7.5	379	1	CYB_FERAT
25	84.5	7.5	379	1	CYB_KOBEL
26	84.5	7.5	379	1	CYB_MUNMU
27	84.5	7.5	379	1	CYB_ZIPCA
28	84.5	7.5	590	1	NUSM_TRYBB
29	84.5	7.5	1159	1	KCH2_HUMAN
30	84.5	7.5	1162	1	KCH2_MOUSE
31	84	7.4	379	1	CYB_VESMU
32	83.5	7.4	379	1	CYB_BUBBU
33	82.5	7.4	379	1	CYB_DUMDD

34	83.5	7.4	379	1	CYB_BUBQU	P92592	bubalus qua
35	83.5	7.4	379	1	CYB_MYONA	Q95629	myotis natt
36	83.5	7.4	423	1	GP83_MOUSE	P30731	mus musculu
37	83	7.3	379	1	CYB_PTEHP	Q8sjz4	pteropus hy
38	83	7.3	470	1	MTR_NEUCR	P38680	neurospora
39	83	7.3	783	1	YAF3_YEAST	P39719	saccharomyc
40	82.5	7.3	274	1	NU2M_DROSE	P29868	drosophila
41	82.5	7.3	274	1	NU2M_DROSI	P29869	drosophila
42	82.5	7.3	380	1	CYB_APOSE	Q9t9i7	apogon semi
43	82.5	7.3	380	1	CYB_NEORH	Q8hlb9	neocytthus r
44	82.5	7.3	380	1	CYB_POLOR	Q95920	polypterus

APPENDICES

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt 42.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	1087	96.0	MTRP	HUMAN	233	1	Q15012	homo sapiens
2	1061	93.7	MTRP	MOUSE	233	1	Q60961	mus musculus
3	191	16.9	LAMS	HUMAN	262	1	Q13571	homo sapiens
4	189	16.7	LAMS	MOUSE	261	1	Q61168	mus musculus
5	103..5	9.1	G22C	DROME	385	1	P58952	drosoφila
6	93	8.2	Y567	BUCAP	413	1	Q8k902	buchnera australis
7	90	8.0	NU2M	DROMA	274	1	P29867	drosoφila
8	89..5	7.9	D3DR	MOUSE	446	1	P30728	mus musculus
9	89..5	7.9	D3DR	RAT	446	1	P19020	rattus norvegicus
10	88	7.8	FIXN	AZOCA	551	1	P98056	azorhizobium
11	87..5	7.7	Y672	METJA	432	1	Q58086	methanococcus
12	87..5	7.7	YDW6	SCHPO	535	1	Q13912	schizosaccharomyces pombe
13	87	7.7	NU2M	DROME	341	1	P03896	drosoφila
14	87	7.7	PKDR	HUMAN	2253	1	Q9ntg1	homo sapiens
15	86..5	7.6	YUW4	CAEEL	112	1	Q20263	caenorhabditis elegans
16	86..5	7.6	KCH2	RAT	1163	1	Q08962	rattus norvegicus
17	85..5	7.6	NU2M	DROYA	341	1	P03895	drosoφila
18	85..5	7.6	CYB	TRASR	379	1	Q9t9b7	tragelaphus
19	85..5	7.6	YG90	HABIN	457	1	P45320	haemophilus
20	85..5	7.6	NUSM	PART	570	1	P15584	paramecium
21	85	7.5	CYB	CAMBA	379	1	Q34028	camelus bactrianus
22	85	7.5	CIO4	HUMAN	695	1	P56696	homo sapiens
23	84..5	7.5	CYB	AKOCU	267	1	P48518	akodon cursor
24	84..5	7.5	CYB	FERAT	379	1	Q9tdn1	feresa attenuata
25	84..5	7.5	CYB	KOBEL	379	1	Q99342	kobus ellipsiprymnus
26	84..5	7.5	CYB	MUNMU	379	1	Q9tdq7	muntiacus reevesi
27	84..5	7.5	CYB	ZIPCA	379	1	Q36262	ziphodus cataphractus
28	84..5	7.5	NUSM	TRYBB	590	1	P04540	trypanosoma
29	84..5	7.5	KCH2	HUMAN	1159	1	Q12809	homo sapiens
30	84..5	7.5	KCH2	MOUSE	1162	1	Q35219	mus musculus
31	84	7.4	CYB	VESMU	379	1	Q957c8	vespertilio
32	83..5	7.4	CYB	BUBBU	379	1	Q33950	bubalus bubalis

RESULT 1	
MTRP_HUMAN	
ID	MTRP_HUMAN
AC	Q15012;
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Lysosomal-associated transmembrane protein 4A (Golgi 4-transmembrane spanning transporter MTP).
DE	LAPTM4A OR MTRP OR KIAA0108.
OS	<i>Homo sapiens</i> (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	
OX	NCBI_TAXID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Bone marrow;
RX	Medline=95308325; PubMed=7788527;
PA	Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S., Tabata S., Ishikawa K.-I., Kawarabayasi Y., Kotani H., Nomura N.;
RA	"Prediction of the coding sequences of unidentified human genes. XII. The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by analysis of cDNA clones from human cell line KG-1.";
RT	DNA Res. 2:37-43 (1-995).
RL	
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Muscle;
RX	Medline=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scheiner A., Schein J.E., Jones S.J.M., Marra M.A.;
RA	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL	
CC	-!- FUNCTION: May function in the transport of nucleosides and/or nucleoside derivatives between the cytosol and the lumen of an intracellular membrane-bound compartment (By similarity).
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. May reside in an intracellular membrane-bound compartment (Potential).
CC	-!- DOMAIN: The C-terminal domain is necessary for retention within intracellular membranes (By similarity).
CC	

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- Event=Alternative initiation;
Comment=2 isoforms, Long (shown here) and Short/Truncated/MTPL1,
may be produced by alternative initiation;
-1- DOMAIN: The C-terminal domain is necessary for retention within
intracellular membranes.

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EMBL; U34259; AAB04938.1;	-.			
MGD; MGI:108017; Laptm4a.				
InterPro; IPR004687; Mtp.				
Pfam; PF03821; Mtp; 1.				
TIGRFAMs; TIGR00799; mtp;	1;			
Transmembrane; Transport;				
CHAIN 1	233	233	233	233
INIT MET	90	90	90	90
TRANSMEM	29	49	49	49
TRANSMEM	82	102	102	102
TRANSMEM	108	128	128	128
TRANSMEM	160	180	180	180
DOMAIN	226	229	229	229
SEQUENCE	233 AA	26857 MW	26857 MW	26857 MW
				CA409AC774ACE4D6E CBC64:

Query	Match	Score	DB	Length
Y	96.0% ; Best Local Similarity Matches 205 ; Conservative	987 ; Pred. 98.1.6e-78 ; 1. Mismatches 1 ;	DB 1 ; Pred. 1.6e-78 ; 0 ;	Length 233 ;
b	1 MVSMSFKNRSDRFYSTRCCGCHVRGTIILGTWIMVNVNLLMAILTVEVTHPNNSMPAV 1 MVSMSFKNRSDRFYSTRCCGCHVRGTIILGTWIMVNVNLLMAILTVEVTHPNNSMPAV			60 60
Y	61 NIQYEVIGNYSSERMANACVLFFAVSVLMFIISSSMLVYGAISYQVGWLIPFFCYRLFDF 61 NIQYEVIGNYSSERMANACVLFFAVSVLMFIISSSMLVYGAISYQVGWLIPFFCYRLFDF			120 120
b	121 VLSCLVAISSLTYLPRIKEYLDQLPDPFVKDDLLALDSCLLFIVLVPFFALFIFKAYLI 121 VLSCLVAISSLTYLPRIKEYLDQLPDPFVKDDLLALDSCLLFIVLVPFFALFIFKAYLI			180 180
Y	181 NCVWNNCYKYINNRNVPEIAVYPAFES 181 NCVWNNCYKYINNRNVPEIAVYPAFEA			206 206
b				

RESULT 2		MTRP_MOUSE		MTRP_MOUSE		STANDARD		PRT;		233 AA.	
Q60961;		15-JUL-1998	(Rel. 36, Created)								
		15-JUL-1998	(Rel. 36, Last sequence update)								
		10-OCT-2003	(Rel. 42, Last annotation update)								
				Lysosomal-associated membrane protein 4A (Golgi 4-transmembrane spanning transporter)	(Mouse transporter protein)						

61	NIQYEVIGNYSSERMA DNACVLFAVSVLMP IISSMLVYGAISYQVG WLIPFFCYRLFDP	120
121	VLSCLVAISSLTYP RICKYLDQLPDPFP YKDDLLALDSSCLL FIVLVFPALFIFKAY LI	180
121	VLSCLVAISSLTYP RICKYLDQLPDPFP YKDDLLALDSSCLL FIVLVFPALFIFKAY LI	180
181	NCVWNCCYKINRN VPEIAYVPAFES	206

Spanning transporter, mouse transporter protein (MIF).
LAPTM4A OR MTRP.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurotamathia; Muridae; Murinae; Mus

RESULT ³
 QAM5_HUMAN
 D LAM5 HUMAN STANDARD; PRT; 262 AA.
 C Q13571; Q13240; Q14698;
 T 15-JUL-1998 (Rel. 36, Created)
 T 15-JUL-1998 (Rel. 36, Last sequence update)
 T 16-OCT-2001 (Rel. 40, Last annotation update)
 E Lysosomal-associated multitransmembrane protein (Retinoic acid-inducible E3 protein) (HA1520).
 E LAPTM5 OR KIAA0085.
 N Homo sapiens (Human).
 S P08320. Vertebrate Chondrocyte Growth Factor 1
 C P08320. Vertebrate Chondrocyte Growth Factor 1

RL Saccharomyces cerevisiae: J. Biol. Chem. 271:9801-9808 (1996).
CC -1- FUNCTION: May function in the transport of nucleosides and/or
CC nucleoside derivatives between the cytosol and the lumen of an
CC intracellular membrane-bound compartment.
CC ENDOCELLULAR LOCATION: Integral membrane protein. May reside in an
CC membrane-bound compartment (Potential). Isoform
CC probably be localized in the plasma membrane.

```
EuKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=Spleen;  
MEDLINE=96299782; PubMed=8661146;  
Adra C.N., Zhu S., Ko J.-L., Guillenmot J.-C., Cuervo A.M.,  
Kobayashi H., Horiuchi T., Lelias J.-M., Rowley J.D., Lim B.;
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